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Figure 1

VH G250

```
        D   V   K   L   V   E   S   G   G   G   L   V   K   L   G   G   S   L   K   L
1     GAC GTG AAG CTC GTG GAG TCT GGG GGA GGC TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC

        S   C   A   A   S   G   F   T   F   S   N   Y   Y   M   S   W   V   R   Q   T
61    TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT AAC TAT TAC ATG TCT TGG GTT CGC CAG ACT
                                          ───────H1───────

        P   E   K   R   L   E   L   V   A   A   I   N   S   D   G   G   I   T   Y   Y
121   CCA GAG AAG AGG CTG GAG TTG GTC GCA GCC ATT AAT AGT GAT GGT GGT ATC ACC TAC TAT
                                      ──────────────H2──────────────

        L   D   T   V   K   G   R   F   T   I   S   R   D   N   A   K   N   T   L   Y
181   CTA GAC ACT GTG AAG GGC CGA TTC ACC ATT TCA AGA GAC AAT GCC AAG AAC ACC CTG TAC
      ────────────────

        L   Q   M   S   S   L   K   S   E   D   T   A   L   F   Y   C   A   R   H   R
241   CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC ACA GCC TTG TTT TAC TGT GCA AGA CAC CGC
                                                                          ──────────

        S   G   Y   F   S   M   D   Y   W   G   Q   G   T   S   V   T   V   S   S
301   TCG GGC TAC TTT TCT ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
      ───────────────H3───────────────
```
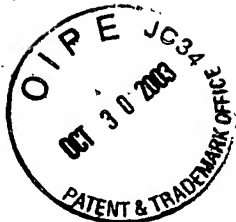
CDRs H1, H2, H3.

CDR definition according to Kabat scheme

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VL G250

```
          D   I   V   M   T   Q   S   Q   R   F   M   S   T   T   V   G   D   R   V   S
  1     GAC ATT GTG ATG ACC CAG TCT CAA AGA TTC ATG TCC ACA ACA GTA GGA GAC AGG GTC AGC

          I   T   C   K   A   S   Q   N   V   V   S   A   V   A   W   Y   Q   Q   K   P
 61     ATC ACC TGC AAG GCC AGT CAG AAT GTT GTT TCT GCT GTT GCC TGG TAT CAA CAG AAA CCA
                          |_____L1_____|

          G   Q   S   P   K   L   L   I   Y   S   A   S   N   R   Y   T   G   V   P   D
121     GGA CAA TCT CCT AAA CTA CTG ATT TAC TCA GCA TCC AAT CGG TAC ACT GGA GTC CCT GAT
                                          |_____L2_____|

          R   F   T   G   S   G   S   G   T   D   F   T   L   T   I   S   N   M   Q   S
181     CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATT AGC AAT ATG CAG TCT

          E   D   L   A   D   F   F   C   Q   Q   Y   S   N   Y   P   W   T   F   G   G
241     GAA GAC CTG GCT GAT TTT TTC TGT CAA CAA TAT AGC AAC TAT CCG TGG ACG TTC GGT GGA
                                      |_____L3_____|

          G   T   K   L   E   I   K
301     GGC ACC AAG CTG GAA ATC AAA
```

CDRs L1, L2, L3
CDR definition according to Kabat scheme

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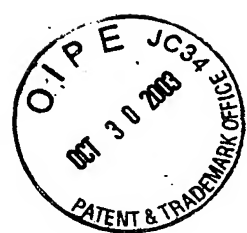Replacement Sheet

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Figure 2

Primers used for PCR amplification of G250 VH and VL regions

5

Anchor and anchor poly C primers:

Anchor: 5'-GCA TGC GCG CGG CCG CGG AGG CC-3'

10   Anchor poly C: 5'-GCA TGC GCG CGG CCG CGG AGG CC(C)$_{12}$-3'

Constant primers:

15   VH-primers: 5'-CTC TAA GCT TGG CTC AAA CAC AGC
                              GAC CTC GGA TAC AGT TGG TGC AGC-3'

VL-primers: 5'-CTC TTC TAG AGA GTC TCT CAG CTG
                              GTA GGA TAC AGT TGG TGC AGC-3'

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Figure 3A

HC_cG250 (EcoRI-fragment in expression vector)   double strand sequencing   08.05.2001

```
   1  TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC CTTTCGTCTT CAAGAATTCT TCAGATACAA AGAATCTCTA AACCCTGAGG ACATTCTATC  100
 101  ACAAATAGT AAATTCAGA AAATTCGAA TGCTCCCATC ACAGAGATGA ATCTGCTATG AACAGCTCAT AGGTGTGAAG CTCTACAAAA GCCATATTAT  200
 201  TGAAAAGCCA CATTGTGCCC AGACTTTGGA AAGACTGAGC TCATATCCTG AAATACAGTT ATGTGTGGTT CTATCTAATT ACACATTTAC ACTAAGGAAA  300
 301  CATGGCAGTA TGGGAATGAA GCTTGTTCTG TACACATTAA CAGAGGGAAA CTAAACAAAG TATGGTGAAT CCCTAACCAA AAGTAAAAAA AAAAAAAAAA  400
 401  AAGAAAGAA AAGAAAAAA AAGTGAAACT ACAATATGTT TCAAATGCTG TAACTGAAAT CTGGTTTTTT GATGCCTTAT ATCTGTTATC ATCAGTGACT  500
 501  TCAGATTTAG TCCAACTCCA GAGCATGGTA TAGCAGGAAG ACATGCAAAT AGGTCTCTC TGTGCCCATG AAAAACACCT CGGCCCTGAC CCTGCAGCTC  600
 601  TGACAGAGGA GGCCTGTCCT GGATTCGATT CCCAGTTCCT CACATTCAGT GATCAGCACT GAACACAGAC CCCTCACCAT GAACTTCGGG CTCAGATTGA  700
 701  TTTTCCTTGT CCTGGTTTTA AAAGGTATCT TATTGAGTAT AGAGGACATC TGCTGTATGC ACAGAGGTGC AGAAAAAATG TTGTTTGTTT TTTTTAGTGA  800
 801  CAATGCTCCA AACAGTATTC TTTCTTTGCA GGTGTCCTGT GTGACGTGAA GCTTGGTGGAG TCTGGGGGAG GCTTAGTGAA GCTTGGAGGG TCCCTGAAAC  900
 901  TCTCCTGTGC AGCCTCTGGA TTCACTTTCA GTAACTTCA  GTTCGCCAGA CTCCAGAGAA GAGGCTGGAG TTGGTCGCAG CCATTAATAG 1000
1001  TGATGGTGGT ATCACCTACT ATCCTAGACAC TGTGAAGGGC TTTCAAGAGA CAATGCCAAG AACACCCTGT ACCTGCAAAT GAGCAGTCTG 1100
1101  AAGTCTGAGG ACACAGGCCT GTTTTACTGT GCAAGACACC GCTCGGGCTA CTTTTCTATG GACTACTGGG GTCAAGGAAC CTCAGTCACC GTCTCCTCAG 1200
1201  GTAAGAATGG CCTCTCCAGG TCTTTTTTTT AATCTTTGTA ATGGAGTTTT CTGAACATTG CAGACTAATC TTGGATATTT GTCCCTGAGG TAGCCGGCTG 1300
1301  ATTATCTCCA CATCTTTGAA AAACTGAGAT TCTGTGTGAT GGTGTTGGTG 1400
1401  GAGTCCCTGG ATGATGGGAT AGGGACTTTG GAGGCTCATT TGAGGGAGAT GCTAAAAACAA TCCTATGGCT GGAGGGAGAG TTGGGGCTGT AGTTGGAGAT 1500
1501  TTTCAGTTTT TAGAATAAAA GCTTTAGCTG TTTGTTGGGA ATGTTCCACA CTAGTTTCTG CCTCTGTGAC AGCATTTATA CAGTATCCGA TGCATAGGA CAAAGAGTGG 1600
1601  AGTGGGGCAC TTTCTTTCGA TTTGTGGGGA GTAGTTGCTG TCCAGAGAGG TGAAACCTCA TTTGTTGGAG GGAGAGCTGT CTTAGTGCCT GAGTCAAGGG 1700
1701  AGAAGGGCAT CTAGCCTTCGG GTAGTTGCTG TCTTAAGTTG GTTCATGTTG TCTGGTTGGAG CCTGCAAAAG TCCAGCTTTC AAAGGAACAC AGAAGTATGT 1800
1801  GTATGGAATA ATAGAAGATG TTGCTTTTAC TCTTTAGTTG GTTCATGTTG AAAAATAGTTA AAACTGTAGG TTTAAAATGT GAGAGGGTTT TCAAGTACTC 1900
1901  ATTTTTTTAC ATGTCCAAAA TTTCTGTCAA TCAATTTGAG GTCTTGTTTG TGTAGAACTG ACATTACTTA AAGTTAACC GAGGAATGGG AGTGAGGCTC 2000
2001  TCTCATACCC TATTCAGAAC TGACTTTTAA CAATAATAAA TTAAGTTTAA AATATTTTTA AATGAATTGA GCAATGTTGA GTTGGAGTCA AGATGGCCGA 2100
```

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LC_cG250 (HindIII-fragment in expression vector)   double strand sequencing   10.05.2001

```
4501 GAGATCTGGG TCTGACTGCA GGTAGCGTGG TCTTCTAGAC GTTTAAGTGG GAGATTTGGG GGGGATGAGG AATGAAGGAA CTTCAGGATA GAAAAGGTCT 4600
4601 GAAGTCAAGT TCAGCTCCTA AAATGGATGT GGGAGCAAAC TTTGAAGATA AACTGAATGA CCCAGAGGAT GAAACAGTGC AGATCAAAGA GGGGCCTGGA 4700
4701 GCTCTGAGAA CAGAAGGAGA GTCATTCGTG TTGAGTTTCC ACAAATACTG TCTTGAGTTT TGCAATAAAA GTGGGATAGC AGAGTTGAGT GAGCCATAGG 4800
4801 CTGAGTTCTC TCTTTTGTCT CCTTAAGTTTT TATGACTACA AAAATCAGTA GTATGTCCTG AAATAATCAT TAAACTGTTT GAAAGTATGA CTGCTTGCCA 4900
4901 TGTAGATACC ATGGCTTGCT GAATAATCAG AAGAGGTGTG ACTCTTATTC TAAAATTTGT CACAAAATGT CAAAATGAGA GACTCTGTAG GAACGAGTCC 5000
5001 TTGACAGACA GCTCAAGGGG TTTTTTTCCT TTGTCTCATT TCTACATGAA AGTAAATTTG AAATGATCTT TTTTATTATA ATAGTAGAAA TACAGTTGGG 5100
5101 TTTGAACTAT ATGTTTTAAT GGCCACGGTT TTGTAAGACA TTTGGCCCTT TGTTTTCCCA GTTATTACTC GCTTGTAATT TTATATCGCC AGCAATGGAC 5200
5201 TGAAACGGTC CGCAACCTCT TCTTTACAAC TGGGTGACCT CGCGGCTGTG CCAGCCATTT GGCGTTCACC TTGCCGCTAA GGGCCGTGTG AACCCCCGAG 5300
5301 GTAGCATCCC TTGCTCCGCG TGGACCACTT TCCTGAGGCA CAGTGATAGG AACAGAGCCA CTAATCTGAA GAGAACAGAG ATGTGACAGA CTACACTAAT 5400
5401 GTTAGAAAAA CAAGGAAAGG GTGACTTATT GGAGATTTCA GAAATAAAAT GCATTTATTA TTATATTCCC TTATTTTAAT TTTCTATTAG GGAATTAGAA 5500
5501 AGGGCATAAA CTGCTTTATC CAGTGTTATA TTAAAAGCTT TTTTTTTTTC AGTGCTA                                                  5557
```

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Figure 3B

LC_cG250 (HindIII-fragment in expression vector)   double strand sequencing   10.05.2001

```
   1 AATTCCAAGC TTTGTATCTT CAGATCCAGG AAAGCCACCA CCAATATCAA   ACAGATACAT GCTGAAACCA ACTTCTGTTC TTATGTCAAA TGCACAGCGG  100
 101 GCATCTGACA CTGCCTGCAT GAAGGTCTCA GGTCAATACT TCCACTACAC   ACATGGAAGC TGACACCAAT GACGTCAATA TTTAGCTCTT TTGCCCATTT  200
 201 CAGGAGGAGA CTGCTGGTTT TGAGTGTGGC ACCAGACTTA ACACCAAGTC   GACAAACTGC TTTGGAATCA TCTGTGACAA TCCACAAAAA CAACTTGTC   300
 301 TTACAATGTG CTCTGACGAC ATTCATCAAT TCATTTCACT GTCAAAAGTC   ATCATCTGGA CTCCAATACT GGCAGCATAC TTGATTTGAG ACACTTGTTT  400
 401 ACAAAAATGT GCATAGGTAA TCCTCTCTGG AGGAACCAGA AGCCCCCGTT   CCAACTGTAT TTCAGTCTTG CTTGCACAGT CAAATCCTGT ACCAATAGCA  500
 501 GCTAGGGTGT TAACTATGGC TCTGTTGTCC TTACACTTGA CTGCACAAAA   AGGAATAACA TTCGGAAGAG CTTTTAGCCA CCTCAGATGC TTCTTTAGAA  600
 601 TGTTCTCTGAG GTCCGGAACC TAGAAAGAAG AGACTTCATT TATTATTTTG   TGTTCAGAAT GTCCTTAGCA CTAAAGCCAC CATCTATGAT ACAGCAGTCA  700
 701 AACTCTTCCT TAGTATAGCT GCTCATCGTT CTCCCATGTGC CTACAGAAAA   CCTAGACATG GAATTAAATT AATTGCCAGCC CCTTACAAGG TCAACTTATC  800
 801 CAAGAACTGT GAATGCAGAC TCCTTGAAAT GTTGGAAACA CTCACAGCAC   AGGGTCAAGA CTGGCTGGAC ACATGGAGAC ACTGAATCCT GAAGAGCACT  900
 901 TAGCTGTCTG TTGCTTCATC ATGTCTACTG ACCTGAGGTG GCACCAAGCT   GCTTACTGAG GGAGGACTGT GGCGGTGTCT GCAGGAACTG ACAATTCTCC 1000
1001 ACAATTCTCT TACTGCCCCA CTCATAACTC TTCTCTTCTC CATCTTCTTC   TTTCTTTCCT CTCCCCTCCT TTTTCCCTTT CACTACTTTT TTCCTTTCTT 1100
1101 CTTTTCCACT TCCCTTTTCT TTCTTCTTTT GCTGTTGCTG TTGTAAAGA    TTTATTGTTT CCTCGTGATT GAACCAAAGG TAGTTGTACT ATTATTTCTG 1200
1201 TAAAACTCAT CTGTTGATTT TCTATTAATT AATTAATTTT GTTTACACTC   CATATTTTAT TCAACCCCTC CATCCTCCTA CTGGTCTACA TACCATACCT 1300
1301 CCTTCCCACA CCCCTGTCTC CACATGGATG CTGCCACCTC CCATGCCACC   TGACCTCTCA TCTCCCTAGG GCATCTAGTC TCTTGAGGCT TAGATGCATC 1400
1401 ATTTCTGAGT GAACACAGAT CCAACAATCC TCTGCTATAT GTGTGTTGGT   GGCCTCATAG CAGCTGGTGT ATGCTGCCTG TTTGTTGATC CAGTGTTTGA 1500
1501 GAGGTCTCGC GGGTTCAGAT TAATTGAGAT TGTTGGACCT CCTCAGCGTC   TTTCAGTCTT TCCCTGATTC AACAACAGGG TTCATTGTTT CTGTTCATTG 1600
1601 GTTGGGGTGCA AATATCTGCA TCTGACTCAG CTGCTTATTG GGTCTTCTGG   AGTGCAGTCA TGCTAGGTCC GTTTCTATGA GTGCTCCATA GCCTCAGTGA 1700
1701 TAGTGTCAGG CGTTGGGACT GCCCCTTGAC CTGGATTCTA TTTTGGACCT   GTCGCTGGAC CTTCTTTTCC TCAGGCTCCC CTCCATCTGT ATCCCTGTAA 1800
1801 TTCTTTCAGA CAGGAACAAA TATGGGTCAG AGTTGTGAGT GTGGAATGGC   ACCCCCTTCC CTCATTTAAT GCCCTGTCTT CCTGGTGGAA GTGGGCTCTA 1900
1901 TAAGTTCCCA CTCCCTACTG TTGGGCATTT CATCCCTTTG AGTCCTGAGA   GTCTCTCACC TCCCAGGTCT CTGGTGCATT CTGGAGGGTC CTCCCAACCT 2000
2001 CCTACCTCCC CAGGTTGCCT GTTGACAGAC TTCTGCTGGC CCCCAGTGCT   TCAGTCCTTT TCCCTCACCC AATATCTGAT TTGGATGGAA GCCTGTCATG 2100
```

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HC_cG250 (EcoRI-fragment in expression vector)   double strand sequencing   08.05.2001

```
2101 TCAGAACCAG AACACCTGCA GCAGCTGGCA GGAAGCAGGT CATGTGGCAA  GGCTATTTGG GGAAGGGAAA ATAAAACCAC TAGGTAAACT TGTAGCTGTG 2200
2201 GTTTGAAGAA GTGGTTTTGA AACACTCTGT CCAGCCCCAC CAAACCGAAA  GTCCAGGCTG AGCAAAACAC CACCTGGGTA ATTTGCATTT CTAAAATAAG 2300
2301 TTGAGGATTC AGCCGAAACT GGAGAGGTCC TCTTTTAACT TATTGAGTTC  AACCTTTTAA TTTTAGCTTG AGTAGTTCTA GTTTCCCCAA ACTTAAGTTT 2400
2401 ATCGACTTCT AAAATGTATT TAGAATTCAT T                                                                          2431
```

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LC_cG250 (HindIII-fragment in expression vector)   double strand sequencing   10.05.2001

```
2101 AGAACATCTA TATACTTGTG GTTTCAGAGC TTTAAATTGG TCCTTGAGCT   TCTATTTTGA GTTCCTTTCC AGTGATTACT TGCTGTCTTT GGTAGTACTT 2200
2201 TTGACTGTTT ATTTAACCTG GATACTCTCA TACAGCTGTG TAATTTACTT   CCTTATTTGA TGACTGCTTT GCATAGATCC CTAGAGGCCA GCCCAGCTGC 2300
2301 CCATGATTTA TAAACCAGGT CTTTGGCAGTG AGATCTGAAA TACATCAGAA   CAGCATGGGC TTCAAGATGG AGTTTCATAC TCAGGTCTTT GTATTCGTGT 2400
2401 TTCTCTGGTT GTCTGGTGAG AATTTTAAAA GTATTATAAC ATCTCAAAAG   TAATTTATTT AAATAGCTTT TCCTATAGGA AGCCAATATT AGGCAGACAA 2500
2501 TGCCATTAGA TAAGACATTT TGGATTCTAA CATTTGTGTC AAAAATCTTT   GTATATATAA GTGTTTACTC ATTATCTATT TCTGATTGCA GGTGTTGATG 2600
2601 GAGACATTGT GATGACCCAG TCTCAAAGAT TCATGTCCAC AACAGTAGGA   GACAGGGTCA GCATCACCTG CAAGGCCAGT CAGAATGTGG TTTCTGCTGT 2700
2701 TGCCTGGTAT CAACAGAAAC CAGGACAATC TCCTAAACTA CTGATTACT    CAGCATCCAA TCGGTACACT GGAGTCCCTG ATCGCTTCAC AGGCAGTGGA 2800
2801 TCTGGGACAG ATTTCACTCT CACCATTAGC AATATGCAGT CTGAAGACCT   GGCTGATTTT TTCTTGTCAAC AATATAGCAA CTATCCGTGG ACGTTCGGTG 2900
2901 GAGGCACCAA GCTGGAAATC AAACGTAAAT AGAATCCAAA CTCTCTTTCT   TCCGTTGTCT ATGTCTGTGG CTTCTATGTC TAAAAATGAT GTAGATATTT 3000
3001 TTTCTCTGAG ACCAGATTCT GTCACTCTCC AAGGCAAAGA TACATAGTCA   CTCCGTAAGC AGAGCTGGGA ATAGGCTAGA CATGTTCTCT GGAGAATGAA 3100
3101 TGCCAGTGTA ATAATTAACA CAAGTGATAG TTTCAGAAAT GCTCAAAGAA   GCAGGGTAGC CTGCCCCTAGA CAAACCTTTA CTTGGTGCTC AGACCATGCT 3200
3201 CAGTTTTTGT ATGGGGGTTG AGTGAAGGGA CACCAGTGTG TGTATACGTT   CGGAGGGGGG ACCAAGCTGG AAATAAAACG TAAGTTGTCT TCTCAACTCT 3300
3301 TGTTCACTGA GTCTAACCTT GTTACTTTGT TCTTTGTTGT GTGTTTTTCT   TAAGGAGATT TCAGGGATGT ATCAAATTCC ATTCTCAGAT CAGGTGTTAA 3400
3401 GGAGGGAAAA CTTGTCCCAC AAGAGGTTGG AATGATTTTC AGGCTAAATT   TTAGGCTTCT AAACCAAAGT CATTAAACTA GGGGAAGAGG GATAATTGTC 3500
3501 TGCCTAGGGA GGGTTTTGTG GAAGTACAGT TAAAGTAGAT CACTGTAAAC   CACATTCAGA GATGGGACCA GACTGGAAAT AAAACCTAAG AACATTTTTG 3600
3601 CTCAACTGCT TGTGAAGTTT TGGTCCCATT GTGTCCTTTG TGTGAGTTTG   TGGTGTTCAT TAGATAAATG AACTATTCCT TGTAACCCAA AACTTAAATA 3700
3701 GACGAGAACC AAAAATCTAG CTACTGTATA AGTTGAGCAA ACAGACTGAC   CTCATGTCAG ATTTGTGGGA GAAATGAGAA AGGAACAGTT TTTCTCTGAA 3800
3801 CTTGGCCTAT CTAACTGGAT CAGCCTCAGG CAGGTTTTTG TAAAGGGGGG   CACAGTGATA TGAATCACTG TCGGCTCGGG GACAAAGTTG 3900
3901 GAAATAAAAC GTAAGTAGAT TTTTGCTCAT TTACTTGTGA CGTTTTTGGTT   CTGTTTTGGGT AACTCGTGTG AATTTGTGAC ATTTTGGCTA AATGAGCCAT 4000
4001 TCCTGGCAAC CTGTGCATCA ATAGAAGATC CCCCAGAAAA GAGTCAGTGT   GAAAGCTGAG CGAAAAACTC GTCTTAGGCT TCTGAGACCA GTTTTGTAAG 4100
4101 GGGAATGTAG AAGAAAGAGC TGGGCTTTTC CTCTGAATTT GGCCCATCTA   GTTGGACTGG CTTCACAGGC AGGTTTTTGT AGAGAGGGGC ATGTCATAGT 4200
4201 CCTCACTGTG GCTCACGTTC GGTGCTGGGA CCAAGCTGGA GCTGAAACGT   AAGTACACTT TTCTTCATCTT TTTTTATGTG TAAGACACAG GTTTTCATGT 4300
4301 TAGGAGTTAA AGTCAGTTCA GAAAATCTTG AGAAAATGGA GAGGGCTCAT   TATCAGTTGA CGTGGCATAC AGTGTCAGAT TTTCTGTTTA TCAAGCTAGT 4400
4401 GAGATTAGGG GCAAAAAGAG GCTTTAGTTG AGAGGAAAGT AATTAATACT   ATGGTTCACCA TCCAAGAGAT TGGACCGGAG AATAAGCATG AGTAGTTATT 4500
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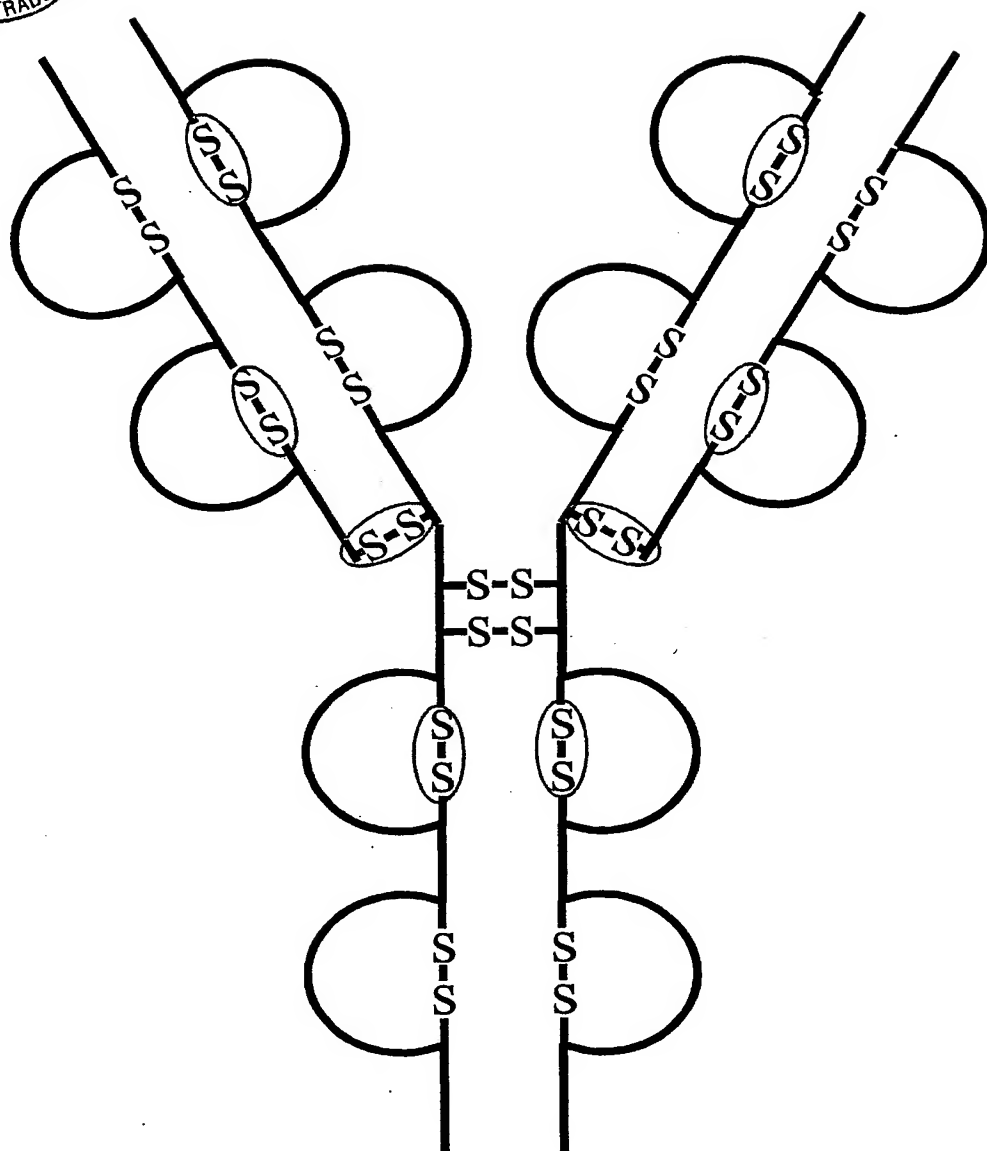. Prel. Amdt. Dated 10/30/03
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Figure 4

Schematic figure of an antibody. Disulfide bonds detected by mass spectrometry after enzymatic digest in WX-G250 are labeled by ovals.

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Figure 5

Characterization of WX-G250 according to MALDI-PMF (Trypsin, LysC, AspN, GluC, and BrCN) in reflector and linear mod

Light Chain:

DIVMTQSQRF MSTTVGDRVS ITCKASQNVV SAVAWYQQKP

GQSPKLLIYS ASNRYTGVPD RFTGSGSGTD FTLTISNMQS

EDLADFFCQQ YSNYPWTFGG GTKLEIKRTV AAPSVFIFPP

SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ

ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG

LSSPVTKSFN RGEC

Heavy Chain:

DVKLVESGGG LVKLGGSLKL SCAASGFTFS NYYMSWVRQT

PEKRLELVAA INSDGGITYY LDTVKGRFTI SRDNAKNTLY

LQMSSLKSED TALFYCARHR SGYFSMDYWG QGTSVTVSSA

STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW

NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP

SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY

VDGVEVHNAK TKPREEQYNSTYRVVSVLTV LHQDWLNGKE

YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL

TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ

KSLSLSPGK

─────────── Reflector mode

- - - - - - - Additional information
              from linear mode spectra

C Detected bridged cysteins (reflector mode)
C Detected bridged cysteins (linear mode)
C: Cystein not determined as bridged cysteins
K Heavy chain partially lacks C-terminal lysine

▓ Confirmed glycosylation site   ✱ Confirmed deamidation sites

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Light chain:

DIVMTQSQRF MSTTVGDRVS ITCKASQNVV SAVAWYQQKP GQSPKLLIYS

ASNRYTGVPD RFTGSGSGTD FTLTISNMQS EDLADFFCQQ YSNYPWTFGG

GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV

DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG

LSSPVTKSFN RGEC

Heavy chain:

DVKLVESGGG LVKLGGSLKL SCAASGFTFS NYYMSWVRQT PEKRLELVAA

INSDGGITYY LDTVKGRFTI SRDNAKNTLY LQMSSLKSED TALFYCARHR

SGYFSMDYWG QGTSVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS

TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK

Figure 6: LC-MS and LC-MS/MS of tryptic digest of cG250